Patent claims

1. Nucleic acid molecule obtainable by starting from a plurality of strains belonging to, on the one hand, a to-be-detected group of bacteria of the *Pseudomonas* genus and, on the other hand, not-to-be-detected bacteria,

(a) isolating, in a manner known *per se*, genomic DNA from a strain of the mentioned bacteria (first strain),

(b) amplifying, in a manner known *per se*, the 23S/5S intergenic region, optionally together with the directly adjacent 23S region and/or the directly adjacent 5S region, and obtaining the amplification product (first amplification product),

(c) in accordance with steps (a) and (b) in each case, isolating genomic DNA using a second, third, . . . and/or n^{th} strain of the mentioned bacteria, amplifying the 23S/5S intergenic region, optionally together with the directly adjacent 23S region and/or the directly adjacent 5S region, and obtaining the amplification product (second, third, . . . n^{th} amplification product),

(d) determining, in a manner known *per se*, the DNA sequence of amplification products obtained according to (b) and (c), and comparing the DNA sequence of the amplification product according to (b) with the DNA sequence of one or more amplification products according to (c), and

(e) obtaining, as a primer or probe, in a manner known *per se*, a nucleic acid molecule by means of which the to-be-detected group of bacteria of the *Pseudomonas* genus can be distinguished from not-to-be-detected bacteria, on the basis of differences at at least one nucleotide position in the sequence region of the nucleic acid molecule.

2. Nucleic acid molecule according to claim 1, obtainable by starting from strains belonging to, on the one hand, to-be-

detected bacteria of the *Pseudomonas* genus and, on the other hand, not-to-be-detected bacteria of a genus (genera) other than *Pseudomonas*.

3. Nucleic acid molecule obtainable by starting from a plurality of strains belonging to a to-be-detected group and a not-to-be-detected group of bacteria of the *Pseudomonas* genus,

(a) isolating, in a manner known *per se*, genomic DNA from a *Pseudomonas* strain of those groups (first strain),

(b) amplifying, in a manner known *per se*, the 23S/5S intergenic region, optionally together with the directly adjacent 23S region and/or the directly adjacent 5S region, and obtaining the amplification product (first amplification product),

(c) in accordance with steps (a) and (b) in each case, isolating genomic DNA using a second, third, . . . and/or n^{th} *Pseudomonas* strain of those groups, amplifying the 23S/5S intergenic region, optionally together with the directly adjacent 23S region and/or the directly adjacent 5S region, and obtaining the amplification product (second, third, . . . n^{th} amplification product),

(d) determining, in a manner known *per se*, the DNA sequence of amplification products obtained according to (b) and (c), and comparing the DNA sequence of the amplification product according to (b) with the DNA sequence of one or more amplification products according to (c), and

(e) obtaining, as a primer or probe, in a manner known *per se*, a nucleic acid molecule by means of which the to-be-detected group of bacteria of the *Pseudomonas* genus can be distinguished from the not-to-be-detected group of bacteria of the *Pseudomonas* genus on the basis of differences at at least one nucleotide position in the sequence region of the nucleic acid molecule.

4. Nucleic acid molecule according to claim 1 or 3, obtainable by starting from strains belonging to a to-be-detected group of bacteria of the species *Pseudomonas aeruginosa* and a not-to-be-detected group of bacteria of other species.

5. Nucleic acid molecule, especially according to one of the preceding claims, of SEQ ID NO 1 or the sequence complementary thereto.

6. Nucleic acid molecule having a shortened sequence compared with a nucleic acid molecule according to claim 5, namely the sequence of the region or in the region of the nucleotide positions 12 to 131.

7. Nucleic acid molecule having a shortened sequence compared with a nucleic acid molecule according to claim 5, namely
(i) SEQ ID NO 3 or
(ii) SEQ ID NO 4 or
(iii) SEQ ID NO 5 or
(iv) the sequence complementary to each of (i), (ii) and (iii).

8. Nucleic acid molecule of SEQ ID NO 2 or the sequence complementary thereto.

9. Nucleic acid molecule ***characterised*** in that, in respect of its sequence in at least ~~10~~ successive nucleotides of its nucleotide chain,
(i) it is identical to a nucleic acid molecule according to one of the preceding claims or

(ii) it corresponds to a nucleic acid molecule according to one of the preceding claims in 9 out of 10 successive nucleotides or

(iii) it corresponds to a nucleic acid molecule according to one of the preceding claims in 8 out of 10 successive nucleotides or

(iv) it is at least 90 % homologous to a nucleic acid molecule according to one of the preceding claims.

10. Nucleic acid molecule according to claim 9, ***characterised*** in that it is from 10 to 250, and preferably from 15 to 30, nucleotides long.

11. Nucleic acid molecule according to ~~one of the preceding claims~~ claim 1, ***characterised*** in that it is single-stranded or double-stranded.

12. Nucleic acid molecule according to ~~one of the preceding claims~~ claim 1, ***characterised*** in that it is present

(i) as DNA or

(ii) as RNA corresponding to (i) or

(iii) as PNA,

the nucleic acid molecule where appropriate having been modified in a manner known *per se* for analytical detection processes, especially those based on hybridisation and/or amplification.

13. Nucleic acid molecule according to claim 12, characterised in that the nucleic acid molecule has been modified in such a manner that up to 20 % of the nucleotides of at least 10 successive nucleotides of its nucleotide chain, especially 1 or 2 nucleotides, have been replaced by analogous building blocks known *per se* as probes and/or

primers, especially by nucleotides that do not occur naturally in bacteria.

14. Nucleic acid molecule according to claim 12 or 13, ***characterised*** in that the nucleic acid molecule has been modified or labelled or additionally modified or labelled in such a manner that it comprises, in a manner known *per se* for analytical detection processes, one or more radioactive groups, coloured groups, fluorescent groups, groups for immobilisation on a solid phase and/or groups for an indirect or direct reaction, especially for an enzymatic reaction, preferably using antibodies, antigens, enzymes and/or substances having an affinity for enzymes or enzyme complexes, and/or otherwise modifying or modified groups of nucleic-acid-like structure.

15. One or more nucleic acid molecules according to ~~one of the preceding claims~~ claim 12 in the presence of optional auxiliary substances and in the form of a kit for analytical detection processes, especially for the detection of bacteria of the *Pseudomonas* genus.

16. Use of one or more nucleic acid molecules according to one of claims 1 to 14 or in the form of a kit according to claim 15 for detection of the presence or absence of bacteria belonging to a group of bacteria of the *Pseudomonas* genus.

17. Use according to claim 16, characterised in that the group of bacteria of the *Pseudomonas* genus includes various strains of *Pseudomonas aeruginosa* or is made up from those strains.

18. Use according to claim 17, characterised in that the group of bacteria of the *Pseudomonas* genus is composed exclusively of *Pseudomonas aeruginosa* strains.

19. Use according to one of claims 16 to 18, ***characterised*** in that nucleic acid hybridisation and/or nucleic acid amplification is/are carried out.

20. Use according to claim 19, ***characterised*** in that, as nucleic acid amplification, a polymerase chain reaction is carried out.

21. Use according to one of claims 16 to 20, ***characterised*** in that the detection is carried out by distinguishing the to-be-detected bacteria from not-to-be-detected bacteria on the basis of differences in the genomic DNA and/or RNA at at least one nucleotide position in the region of a nucleic acid molecule according to one of claims 1 to 14.

22. Use according to claim 21, ***characterised*** in that distinguishing is carried out on the basis of differences in the region of a nucleic acid molecule according to claim 5.